SCORE Search Results Details for Application 10563896 and Search Result 20080416_145120_us-10-563-896-3.rag.

This page gives you Search Results detail for the Application 10563896 and Search Result 20080416_145120_us-10-563-896-3.rag.

```
                         GenCore version 6.2.1
              Copyright (c) 1993 - 2008  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:         April 16, 2008, 14:55:47 ; Search time 120 Seconds
                                           (without alignments)
                                           1705.326 Million cell updates/sec

Title:          US-10-563-896-3
Perfect score:  1807
Sequence:       1 MGKSKEISQDLRKKIVDLHK..........EGYPKRLTQVKQFKGNATKY 340

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       3405708 seqs, 601879884 residues

Total number of hits satisfying chosen parameters:     3405708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      A_Geneseq_200711:*
                1:  geneseqp1980s:*
                2:  geneseqp1990s:*
                3:  geneseqp2000:*
                4:  geneseqp2001:*
                5:  geneseqp2002:*
                6:  geneseqp2003a:*
                7:  geneseqp2003b:*
                8:  geneseqp2004a:*
                9:  geneseqp2004b:*
                10: geneseqp2005:*
                11: geneseqp2006:*
                12: geneseqp2007:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
```

and is derived by analysis of the total score distribution.

SUMMARIES

```
              %
           Query
Result     Match
  No.  Score Match Length DB  ID                    Description
  -----------------------------------------------------------------------------
     1   1807  100.0   340   2  AAW68520            Aaw68520 Salmonid-
     2   1807  100.0   340   2  AAY17440            Aay17440 SB transp
     3   1807  100.0   340   4  AAY72024            Aay72024 SB (Sleep
     4   1807  100.0   340   5  AAG80595            Aag80595 Sleeping
     5   1807  100.0   340   5  ABB07570            Abb07570 SB transp
     6   1807  100.0   340   6  ABB99719            Abb99719 Amino aci
     7   1807  100.0   340   7  ADD41924            Add41924 Amino aci
     8   1807  100.0   340  10  ADW22678            Adw22678 Sleeping
     9   1807  100.0   340  10  ADW03280            Adw03280 Sleeping
    10   1807  100.0   340  11  AEF81669            Aef81669 Salmonid
    11   1807  100.0   340  12  AEP47151            Aep47151 SB transp
    12   1802   99.7   340   7  ADK17480            Adk17480 Salmonid
    13   1787   98.9   340  11  AEF81683            Aef81683 Salmonid
    14   1786   98.8   340   4  AAB47211            Aab47211 Sleeping
    15   1786   98.8   340  10  ADW46561            Adw46561 Salmonid
    16   1786   98.8   340  12  AEL92393            Ael92393 Sleeping
    17   1784   98.7   340  11  AEF81684            Aef81684 Salmonid
    18   1783   98.7   340  10  ADW46599            Adw46599 Salmonid
    19   1783   98.7   340  10  ADW46649            Adw46649 Salmonid
    20   1783   98.7   340  10  ADW46612            Adw46612 Salmonid
    21   1783   98.7   340  10  ADW46621            Adw46621 Salmonid
    22   1783   98.7   340  10  ADW46613            Adw46613 Salmonid
    23   1782   98.6   340  10  ADW46626            Adw46626 Salmonid
    24   1782   98.6   340  10  ADW46644            Adw46644 Salmonid
    25   1782   98.6   340  10  ADW46614            Adw46614 Salmonid
    26   1782   98.6   340  10  ADW46597            Adw46597 Salmonid
    27   1782   98.6   340  10  ADW46587            Adw46587 Salmonid
    28   1781   98.6   340  10  ADW46656            Adw46656 Salmonid
    29   1781   98.6   340  10  ADW46591            Adw46591 Salmonid
    30   1781   98.6   340  10  ADW46643            Adw46643 Salmonid
    31   1781   98.6   340  10  ADW46658            Adw46658 Salmonid
    32   1781   98.6   340  10  ADW46588            Adw46588 Salmonid
    33   1781   98.6   340  10  ADW46605            Adw46605 Salmonid
    34   1781   98.6   340  10  ADW46603            Adw46603 Salmonid
    35   1781   98.6   340  10  ADW46653            Adw46653 Salmonid
    36   1781   98.6   340  10  ADW46607            Adw46607 Salmonid
    37   1781   98.6   340  10  ADW46615            Adw46615 Salmonid
    38   1781   98.6   340  10  ADW46617            Adw46617 Salmonid
    39   1781   98.6   340  10  ADW46590            Adw46590 Salmonid
    40   1781   98.6   340  10  ADW46593            Adw46593 Salmonid
    41   1781   98.6   340  10  ADW46608            Adw46608 Salmonid
    42   1781   98.6   340  10  ADW46645            Adw46645 Salmonid
    43   1781   98.6   340  10  ADW46601            Adw46601 Salmonid
    44   1781   98.6   340  10  ADW46610            Adw46610 Salmonid
    45   1781   98.6   340  10  ADW46630            Adw46630 Salmonid
```

ALIGNMENTS

RESULT 1
AAW68520
ID   AAW68520 standard; protein; 340 AA.
XX

```
AC    AAW68520;
XX
DT    27-AUG-2003  (revised)
DT    25-JAN-1999  (first entry)
XX
DE    Salmonid-type Tc1-like transposase protein.
XX
KW    Transposase; salmonid; Tc1-like family; homology; vertebrate; transposon;
KW    zebrafish; gene transfer; gene therapy; inverted repeat; direct repeat;
KW    genome.
XX
OS    transposons.
XX
FH    Key            Location/Qualifiers
FT    Domain         11. .61
FT                   /note= "Paired-like domain with Leucine Zipper"
FT    Domain         104. .105
FT                   /note= "form part of a bipart nuclear localisation
FT                   signal"
FT    Domain         116. .120
FT                   /note= "form part of a bipart nuclear localisation
FT                   signal"
FT    Domain         151. .161
FT                   /note= "DD(34)E box"
FT    Region         183. .198
FT                   /note= "Glycine-rich box"
FT    Domain         241. .251
FT                   /note= "DD(34)E box"
FT    Domain         268. .282
FT                   /note= "DD(34)E box"
XX
PN    WO9840510-A1.
XX
PD    17-SEP-1998.
XX
PF    11-MAR-1998;   98WO-US004687.
XX
PR    11-MAR-1997;   97US-0040664P.
PR    28-JUL-1997;   97US-0053868P.
PR    13-NOV-1997;   97US-0065303P.
XX
PA    (MINU ) UNIV MINNESOTA.
XX
PI    Hackett PB,  Ivics Z,  Izsvak Z,  Caldovic L;
XX
DR    WPI; 1998-531525/45.
DR    N-PSDB; AAV33841.
XX
PT    New isolated transposase gene - used to develop products for the
PT    integration of nucleic acid fragments into the nucleic acid of cells,
PT    particularly for gene therapy.
XX
PS    Disclosure; Fig 2B; 79pp; English.
XX
CC    This sequence represents a novel transposase protein of the salmonid-type
CC    Tc1-like family. The coding sequence was reconstructed based on sequence
CC    homology between members of the Tc1-like family of vertebrate
CC    transposons, especially based on the sequence of a number of fish, e.g.
CC    zebrafish transposons. The transposase can be used in a gene transfer
CC    method, especially for gene therapy treatment, by flanking a heterologous
CC    gene to be expressed in a cell with the inverted or direct repeat
```

```
CC    sequences to which the transposase binds. This allows the transposase-
CC    mediated transposition of the heterologous into the genome of the host
CC    cell. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ    Sequence 340 AA;

   Query Match              100.0%;  Score 1807;  DB 2;  Length 340;
   Best Local Similarity    100.0%;  Pred. No. 2.4e-156;
   Matches  340;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MGKSKEISQDLRKKIVDLHKSGSSLGAISKRLKVPRSSVQTIVRKYKHHGTTQPSYRSGR 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MGKSKEISQDLRKKIVDLHKSGSSLGAISKRLKVPRSSVQTIVRKYKHHGTTQPSYRSGR 60

Qy       61 RRVLSPRDERTLVRKVQINPRTTAKDLVKMLEETGTKVSISTVKRVLYRHNLKGRSARKK 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 RRVLSPRDERTLVRKVQINPRTTAKDLVKMLEETGTKVSISTVKRVLYRHNLKGRSARKK 120

Qy      121 PLLQNRHKKARLRFATAHGDKDRTFWRNVLWSDETKIELFGHNDHRYVWRKKGEACKPKN 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 PLLQNRHKKARLRFATAHGDKDRTFWRNVLWSDETKIELFGHNDHRYVWRKKGEACKPKN 180

Qy      181 TIPTVKHGGGSIMLWGCFAAGGTGALHKIDGIMRKENYVDILKQHLKTSVRKLKLGRKWV 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TIPTVKHGGGSIMLWGCFAAGGTGALHKIDGIMRKENYVDILKQHLKTSVRKLKLGRKWV 240

Qy      241 FQMDNDPKHTSKVVAKWLKDNKVKVLEWPSQSPDLNPIENLWAELKKRVRARRPTNLTQL 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 FQMDNDPKHTSKVVAKWLKDNKVKVLEWPSQSPDLNPIENLWAELKKRVRARRPTNLTQL 300

Qy      301 HQLCQEEWAKIHPTYCGKLVEGYPKRLTQVKQFKGNATKY 340
            ||||||||||||||||||||||||||||||||||||||||
Db      301 HQLCQEEWAKIHPTYCGKLVEGYPKRLTQVKQFKGNATKY 340
```